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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Schlessinger, Joseph  
Sap, Jan M.

(ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
PHOSPHATASE-ALPHA

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PENNIE & EDMONDS  
(B) STREET: 1155 AVENUE OF THE AMERICAS  
(C) CITY: NEW YORK  
(D) STATE: NEW YORK  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/015,985  
(B) FILING DATE: 10-FEB-1993  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.  
(B) REGISTRATION NUMBER: 30,742  
(C) REFERENCE/DOCKET NUMBER: 7683-020

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 802 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys  
1 5 10 15

Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr  
20 25 30

Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Ala Lys  
35 40 45

Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr  
50 55 60

Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn  
65 70 75 80

Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser  
85 90 95

Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln  
100 105 110

Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala  
115 120 125

Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys  
130 135 140

Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser  
145 150 155 160

Ser Leu Leu Val Ile Val Phe Ile Ile Val Leu Tyr Met Leu Arg  
165 170 175

Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu  
180 185 190

Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu  
195 200 205

Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp  
210 215 220

Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu  
225 230 235 240

Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr  
245 250 255

Cys Glu Ala Ala Ser Lys Glu Asn Lys Glu Lys Asn Arg Tyr Val  
260 265 270

Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu  
275 280 285

Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr  
290 295 300

Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr  
305 310 315 320

Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile  
325 330 335

Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln  
340 345 350

Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser  
355 360 365

Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys  
370 375 380

Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile  
385 390 395 400

Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr  
405 410 415

Pro Ile Gly Met Leu Lys Phe Leu Lys Val Lys Ala Cys Asn Pro

420

425

430

Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg  
435 440 445

Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr  
450 455 460

Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln  
465 470 475 480

Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln  
485 490 495

Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr  
500 505 510

Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr  
515 520 525

Ser Asn Asn Gly Leu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys  
530 535 540

Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys  
545 550 555 560

Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile  
565 570 575

Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val Asn Ala Ser  
580 585 590

Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly  
595 600 605

Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp  
610 615 620

Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu Arg Gly Gln  
625 630 635 640

Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly  
645 650 655

Asp Ile Thr Val Glu Leu Lys Glu Glu Glu Cys Glu Ser Tyr Thr  
660 665 670

Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln  
675 680 685

Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser  
690 695 700

Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln  
705 710 715 720

Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala  
725 730 735

Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val  
740 745 750

Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg  
755 760 765

Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys  
770 775 780

Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn  
785 790 795 800

Phe Lys

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGATTCTT	GGTTCAATTCT	TGTTCTGCTC	GGCAGTGGTC	TGATATGTGT	CAGTGCCAAAC	60
AATGCTACCA	CAGTTGCACC	TTCTGTAGGA	ATTACAAGAT	TAATTAACTC	ATCAACGGCA	120
GAACCCAGTTA	AAGAAGAGGC	CAAAAACCTCA	AATCCAACCTT	CTTCACTAAC	TTCTCTTCT	180
GTGGCACCAA	CATTCAAGCCC	AAATATAACT	CTGGGACCCA	CCTATTAAAC	CACTGTCAAT	240
TCTTCAGACT	CTGACAAATGG	GACCACAAGA	ACAGCAAGCA	CCAATTCTAT	AGGCATTACA	300
ATTTCACCAA	ATGGAACGTG	GCTTCCAGAT	AACCAGTTCA	CGGATGCCAG	AACAGAACCC	360
TGGGAGGGGA	ATTCCAGCAC	CGCAGCAACC	ACTCCAGAAA	CTTCCCTCC	TTCAGGTAAT	420
TCTGACTCGA	AGGACAGAAG	AGATGAGACA	CCAATTATTG	CGGTGATGGT	GGCCCTGTCC	480
TCTCTGCTAG	TGATCGTGT	TATTATCATA	GTTTGTACA	TGTTAACGTT	TAAGAAATAC	540
AAGCAAGCTG	GGAGCCATT	CAATTCTTC	CGCTTATCCA	ACGGCCGCAC	TGAGGATGTG	600
GAGCCCCAGA	GTGTGCCACT	TCTGGCCAGA	TCCCCAAGCA	CCAACAGGAA	ATACCCACCC	660
CTGCCCCGTGG	ACAAGCTGGA	AGAGGAATT	AACGGGAGAA	TGGCAGACGA	CAATAAGCTC	720
TTCAGGGAGG	AATTCAACGC	TCTCCCTGCA	TGTCTTATCC	AGGCCACCTG	TGAGGCTGCT	780
TCCAAGGAGG	AAAACAAGGA	AAAAAATCGA	TATGTAAACA	TCTTGCCTTA	TGACCACTCT	840
AGAGTCCACC	TGACACCGGT	TGAAGGGTT	CCAGATTCTG	ATTACATCAA	TGCTTCATTC	900
ATCAACGGTT	ACCAAGAAAA	GAACAAATT	ATTGCTGCAC	AAGGACCAAA	AGAAGAAACG	960
GTGAATGATT	TCTGGCGGAT	GATCTGGAA	CAAAACACAG	CCACCATCGT	CATGGTTACC	1020
AACCTGAAGG	AGAGAAAGGA	GTGCAAGTGC	GCCCAGTACT	GGCCAGACCA	AGGCTGCTGG	1080
ACCTATGGGA	ATATTGGGT	GTCTGTAGAG	GATGTGACTG	TCCTGGTGG	CTACACAGTA	1140
CGGAAGTTCT	GCATCCACCA	GGTGGCGAC	ATGACCAACA	GAAAGCCACA	GCGCCTCATC	1200
ACTCAGTTCC	ACTTTACCAAG	CTGGCCAGAC	TTTGGGTGC	CTTTTACCCC	GATCGGCATG	1260
CTCAAGTTCC	TCAAGAAGGT	GAAGGCCTGT	AACCCTCAGT	ATGCAGGGGC	CATCGTGGTC	1320
CACTGCAGTG	CAGGTGTAGG	GCGTACAGGT	ACCTTGTGCG	TCATTGATGC	CATGCTGGAC	1380
ATGATGCATA	CAGAACGGAA	GGTGGACGTG	TATGGCTTG	TGAGCCGGAT	CCGGGCACAG	1440
CGCTGCCAGA	TGGTGCAAAC	CGATATGCAG	TATGTCTTCA	TATACCAAGC	CCTTCTGGAG	1500

CATTATCTCT ATGGAGATAAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA	1560
ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA	1620
ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCAGC CAACATGAAG	1680
AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCAACA GAGTGTACAT TCCAGTTAAG	1740
CGGGGCGAAG AGAATACAGA CTATGTAAAC GCATCCTTTA TTGATGGCTA CCCGCAGAAG	1800
GACTCCTATA TCGCCAGGCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG	1860
ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG	1920
GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGACTGGTGT CCTATGGAGA TATTACAGTG	1980
GAACGTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTCACCAAC	2040
ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG	2100
GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG	2160
CAGCAGTCAG GGAACCACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG	2220
ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGAT TTTGGATGTC	2280
TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG	2340
TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC	2400
TTCAAGTAA	2409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His  
1 5 10 15

Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr  
20 25 30

Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys  
35 40 45

Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr  
50 55 60

Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn  
65 70 75 80

Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser  
85 90 95

Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln  
100 105 110

Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala  
115 120 125

Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile  
130 135 140

Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile  
145 150 155 160

Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser  
165 170 175

His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu  
180 185 190

Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys  
195 200 205

Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg  
210 215 220

Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro  
225 230 235 240

Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn  
245 250 255

Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg  
260 265 270

Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn  
275 280 285

Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala  
290 295 300

Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp  
305 310 315 320

Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu Arg  
325 330 335

Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Cys Trp Thr  
340 345 350

Tyr Gly Asn Val Arg Val Ser Val Glu Asp Val Thr Val Leu Val Asp  
355 360 365

Tyr Thr Val Arg Lys Phe Ser Ile Gln Gln Val Gly Asp Val Thr Asn  
370 375 380

Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp Pro  
385 390 395 400

Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys  
405 410 415

Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val His  
420 425 430

Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp Ala  
435 440 445

Met Leu Asp Met Met His Ser Glu Arg Lys Val Asp Val Tyr Gly Phe  
450 455 460

Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp Met  
465 470 475 480

Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu His Tyr Leu Tyr Gly

485

490

495

Asp Thr Glu Leu Glu Val Thr Ser Leu Glu Thr His Leu Gln Lys Ile  
500 505 510

Tyr Asn Lys Ile Pro Gly Thr Ser Asn Asn Gly Leu Glu Glu Glu Phe  
515 520 525

Lys Lys Leu Thr Ser Ile Lys Ile Gln Asn Asp Lys Met Arg Thr Gly  
530 535 540

Asn Leu Pro Ala Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro  
545 550 555 560

Tyr Glu Phe Asn Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn  
565 570 575

Thr Asp Tyr Val Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp  
580 585 590

Ser Tyr Ile Ala Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe  
595 600 605

Trp Arg Met Ile Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr  
610 615 620

Glu Leu Glu Glu Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser  
625 630 635 640

Asp Gly Leu Val Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu  
645 650 655

Glu Glu Cys Glu Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr  
660 665 670

Arg Glu Asn Lys Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp  
675 680 685

Pro Glu Val Gly Ile Pro Ser Asp Gly Lys Gly Met Ile Asn Ile Ile  
690 695 700

Ala Ala Val Gln Lys Gln Gln Gln Ser Gly Asn His Pro Ile Thr  
705 710 715 720

Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu  
725 730 735

Ser Thr Val Leu Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe  
740 745 750

Gln Thr Val Lys Ser Leu Arg Leu Gln Arg Pro His Met Val Gln Thr  
755 760 765

Leu Glu Gln Tyr Glu Phe Cys Tyr Lys Val Val Gln Glu Tyr Ile Asp  
770 775 780

Ala Phe Ser Asp Tyr Ala Asn Phe Lys  
785 790

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2872 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCGGC GAGTGAGGCG CTGACAGGGG CTCGCGGGGG CATCTTGCAC AGACCCCTGG	60
ACCACGCCGC CATCGCAGCC TCCAGCCCAG TCCTCTCTCT GCCGCTCTC CTCGCCATGG	120
AGGCCGCCGA CCGCCGTCCG CGGGCTTCGA GCAGCGGACC GGGCCGGGCT GACCCCATGT	180
GGGCCGAGAG CCCGGTCGTG AGGCCGAGCT GCCGTGCGCG TCCCCCGGG TCCCGCCCCA	240
GCGCCGGGCT CGGTCAGCAT GGATTCCCTGG TTCATTCTTG TCCTGTTGG CAGTGGTCTA	300
ATACATGTTA GTGCCAACAA TGCTACTACA GTTTCACCTT CTTTAGGAAC GACAAGATTA	360
ATTAAAAACAT CAACAACAGA ATTGGCTAAG GAAGAGAATA AAACCTCAA TTCAACCTCT	420
TCAGTAATTCTCTGT GGCACCAACA TTCAGCCCAA ACCTGACTCT GGAGCCCAACC	480
TATGTGACTA CTGTTAATTC TTCACACTCT GACAATGGGA CCAGGAGGGC AGCCAGCAGG	540
GAATCTGGAG GCACTACCAT TTCCCCGAAC GGAAGCTGGC TTATTGAGAA CCAGTTCACCG	600
GATGCCATAA CAGAACCTTG GGAGGGGAAC TCCAGCACTG CAGCAACCAC TCCAGAAACC	660
TTCCCCCGG CAGATGAGAC ACCAATTATT GCGGTGATGG TGGCCCTGTC CTCTCTGCTA	720
GTAATCGTGT TTATTATCAT AGTTCTGTAC ATGTTAAGGT TTAAGAAATA CAAGCAAGCT	780
GGGAGTCATT CCAACTCTTT CCGCCTGTCA AATGGCCGCA CGGAGGATGT GGAGCCCAA	840
AGTGTACAC TTCTGGCCAG GTCCCCGAGC ACCAACAGGA AGTACCCACC ACTGCCTGTG	900
GACAAGCTGG AAGAGGAGAT TAACCGGAGA ATGGCTGATG ACAATAAGCT CTTCAGAGAA	960
GAATTCAACG CTCTCCCTGC TTGTCCTATC CAGGCCACCT GTGAGGCTGC CTCCAAGGAA	1020
GAAAACAAGG AAAAAAACCG CTATGTAAAC ATCCTGCCCT ATGACCACTC TAGAGTGCAC	1080
CTGACACCTG TTGAAGGGGT CCCAGATTCT GATTACATCA ACGCTTCATT CATTAAATGGC	1140
TACCAGGAAA AGAACAAATT CATCGCTGCA CAAGGACCAA AAGAAGAAC AGTGAATGAC	1200
TTCTGGAGAA TGATATGGGA ACAAAACACA GCTACTATTG TCATGGTGAC CAACCTGAAG	1260
GAGAGAAAGG AGTGTAAATG TGCCCAATAC TGGCCAGACC AAGGCTGCTG GACCTATGGG	1320
AATGTCCGTG TGTCTGTGCA GGATGTGACT GTTCTGGTGG ACTACACAGT ACGGAAATTC	1380
TCGATCCAGC AGGTGGCGA CGTGACCAAC AGGAAACCAC AGCGCCTCAT CACTCAGTTC	1440
CACTTCACCA GCTGGCCAGA CTTTGGGTG CCTTTCACCC CAATTGGCAT GCTCAAGTTC	1500
CTCAAGAAGG TGAAGGCCTG TAACCCCTCAG TACGCAGGGG CTATCGTGGT CCACTGCAGT	1560
GCAGGTGTAG GGCGCACTGG CACCTTGTT GTCATCGATG CCATGCTGGA CATGATGCAT	1620
TCGGAGCGCA AAGTGGATGT ATATGGGTTT GTGAGCCGGA TCCGGGCCCA GCGCTGCCAG	1680
ATGGTACAGA CAGACATGCA GTACGTCTTC ATATACCAAGG CCCTTCTGGA GCATTATCTG	1740
TATGGGGACA CAGAACTGGA AGTGAACCTCT CTAGAAACCC ACCTACAAAA AATTATAAC	1800
AAGATCCCAG GGACTAGCAA CAACGGGTTA GAGGAGGAGT TTAAGAAATT AACTTCAATC	1860
AAAATCCAGA ATGACAAGAT GCGCACGGGA AACCTTCCAG CCAACATGAA GAAGAACCGG	1920

GTTTTACAGA TCATTCCATA TGAATTAAAC AGAGTGATCA TTCCAGTCAA ACGAGGCGAA	1980
GAGAACACAG ACTATGTGAA CGCATCCTTC ATTGATGGAT ACCGGCAGAA AGACTCCTAC	2040
ATTGCCAGCC AGGGCCCTCT TCTCCACACG ATTGAGGACT TCTGGCAAT GATCTGGAG	2100
TGGAAGTCCT GTTCTATCGT AATGCTGACA GAACTGGAAG AGAGAGGCCA GGAGAAGTGT	2160
GCCCCAGTACT GCCCATCTGA TGGCCTGGTG TCCTACGGAG ACATCACAGT TGAGCTGAAG	2220
AAGGAGGAGG AATGTGAAAG CTACACTGTC CGAGACCTCC TGGTCACCAA CACCAGGGAG	2280
AACAAGAGTC GGCAAATCCG GCAGTTCCAC TTCCACGGCT GGCCTGAGGT GGGCATCCCC	2340
AGCGACGGCA AGGGCATGAT CAACATCATT GCAGCAGTGC AGAAGCAGCA GCAGCAGTCG	2400
GGGAACCATC CCATCACTGT GCACTGCAGT GCGGGGGCAG GACGGACAGG AACCTTCTGT	2460
GCCTTGAGCA CAGTCCTGGA ACGTGTGAAA GCAGAAGGAA TTTTAGATGT CTTCCAAACT	2520
GTCAAGAGCC TGCGGCTGCA GAGGCCACAC ATGGTCCAGA CACTGGAACA GTATGAATT	2580
TGCTACAAAGG TGGTACAGGA ATACATTGAC GCCTTTTCAG ATTATGCCAA CTTCAAGTGA	2640
CAGGTGACAA GGCCCACAGA CAGGAGAATT GCCTTTAATA TTTTGTAAATA TTCTGTTTT	2700
GTAAATATAC CCAAAATTGT ATATATCTTA TAACTGTTTT AGAAATGGCA CATAGGCTTC	2760
TATTACCTGT TAGATGGAGA TTTGTATGT AAATGTGTTA GCACTGATAG TCCTTTCCA	2820
GTGTTTATT GGGAAATTAA TAGTGTGATA TTTGGGTTGA TATAATGAAT TC	2872

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu Pro Tyr Asp Tyr Asn  
1 5 10 15

Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala Gly Ser Asn Tyr Ile  
20 25 30

Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro Arg Lys Tyr Ile Ala  
35 40 45

Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp Phe Trp Arg Met Ile  
50 55 60

Trp Glu Gln Lys Ala Thr Val Ile Val Met Val Thr Arg Cys Glu Glu  
65 70 75 80

Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro Ser Met Glu Glu Gly  
85 90 95

Thr Arg Ala Phe Gly Asp Val Val Lys Ile Asn Gln His Lys Arg  
100 105 110

Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile Val Asn Lys Lys Glu

115	120	125
Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser Trp Pro		
130	135	140
Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys Leu Arg Arg		
145	150	155
Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val Val His		
165	170	175
Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile Asp Ala		
180	185	190
Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr Gly Tyr		
195	200	205
Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val Glu Ala		
210	215	220
Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser		
1	5	10
15		
Arg Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile		
20	25	30
Asn Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala		
35	40	45
Ala Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile		
50	55	60
Trp Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu		
65	70	75
80		
Arg Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Glu Trp		
85	90	95
Thr Tyr Gly Asn Ile Arg Val Ser Val Glu Asp Val Thr Val Leu Val		
100	105	110
Asp Tyr Thr Val Arg Lys Phe Cys Ile Gln Gln Val Gly Asp Met Thr		
115	120	125
Asn Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp		
130	135	140
Pro Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu		
145	150	155
160		
Lys Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val		

165

170

175

His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp  
180 185 190

Ala Met Leu Asp Met Met His Thr Glu Arg Lys Val Asp Val Tyr Gly  
195 200 205

Phe Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp  
210 215 220

Met Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu  
225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser  
1 5 10 15

Arg Val Lys Leu Ala Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp  
20 25 30

Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr  
35 40 45

Ile Ala Ala Gln Gly Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg  
50 55 60

Met Ile Trp Glu His Asn Val Glu Val Ile Val Met Ile Thr Asn Leu  
65 70 75 80

Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly  
85 90 95

Ser Glu Glu Tyr Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val  
100 105 110

Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile  
115 120 125

Lys Lys Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln  
130 135 140

Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu  
145 150 155 160

Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His Ala  
165 170 175

Val Gly Pro Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly  
180 185 190

Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln His Glu Gly  
195 200 205

Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn

210

215

220

Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Thr Leu  
225 230 235 240

Val Glu

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Leu Ala Tyr Asp His Ser  
1 5 10 15

Arg Val Lys Leu Arg Pro Leu Pro Gly Lys Asp Ser Lys His Ser Asp  
20 25 30

Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Lys Ala Lys Ala Tyr  
35 40 45

Ile Ala Thr Gln Gly Pro Leu Lys Ser Thr Phe Glu Asp Phe Trp Arg  
50 55 60

Met Ile Trp Glu Gln Asn Thr Gly Ile Ile Val Met Ile Thr Asn Leu  
65 70 75 80

Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Thr Glu Asn  
85 90 95

Ser Glu Glu Tyr Gly Asn Ile Ile Val Thr Leu Lys Ser Thr Lys Ile  
100 105 110

His Ala Cys Tyr Thr Val Arg Arg Phe Ser Ile Arg Asn Thr Lys Val  
115 120 125

Lys Lys Gly Gln Lys Gly Asn Pro Lys Gly Arg Gln Asn Glu Arg Val  
130 135 140

Val Ile Gln Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu  
145 150 155 160

Tyr Ala Leu Pro Val Leu Thr Phe Val Arg Arg Ser Ser Ala Ala Arg  
165 170 175

Met Pro Glu Thr Gly Pro Val Leu Val His Cys Ser Ala Gly Val Gly  
180 185 190

Arg Thr Gly Thr Tyr Ile Val Ile Asp Ser Met Leu Gln Gln Ile Lys  
195 200 205

Asp Lys Ser Thr Val Asn Val Leu Gly Phe Leu Lys His Ile Arg Thr  
210 215 220

Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Ile Phe Ile His  
225 230 235 240

Asp Ala Leu Leu Glu  
245

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: /label= Xaa  
*/note= "For the Consensus Sequence, Xaa = Lack of Consensus"*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn Lys His Lys Asn Arg Tyr Xaa Asn Ile Leu Xaa Tyr Asp His Ser  
1 5 10 15

Arg Val Lys Leu Xaa Xaa Leu Xaa Xaa Lys Xaa Xaa Lys Xaa Ser Asp  
20 25 30

Tyr Ile Asn Ala Xaa Tyr Xaa Asp Gly Tyr Asn Glu Pro Lys Xaa Tyr  
35 40 45

Ile Ala Ala Gln Gly Pro Leu Lys Xaa Thr Val Glu Asp Phe Trp Arg  
50 55 60

Met Ile Trp Glu Gln Asn Thr Xaa Val Ile Val Met Xaa Thr Asn Leu  
65 70 75 80

Val Glu Lys Gly Arg Arg Lys Cys Xaa Gln Tyr Trp Pro Xaa Xaa Gly  
85 90 95

Ser Glu Xaa Tyr Gly Asn Ile Xaa Val Thr Val Lys Xaa Val Xaa Val  
100 105 110

Leu Ala Xaa Xaa Asp Tyr Thr Val Arg Lys Phe Xaa Xaa Arg Asn Thr  
115 120 125

Lys Ile Xaa Lys Xaa Gly Xaa Lys Xaa Xaa Xaa Lys Gly Arg Xaa Xaa  
130 135 140

Gly Arg Val Val Thr Gln Tyr His Xaa Thr Xaa Trp Pro Asp Met Gly  
145 150 155 160

Val Pro Glu Tyr Pro Leu Pro Val Leu Xaa Phe Val Arg Xaa Val Xaa  
165 170 175

Ala Ala Xaa Xaa Xaa Xaa Gly Pro Xaa Val Val His Cys Ser Ala  
180 185 190

Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Ile Asp Xaa Met Leu Gln  
195 200 205

Gln Ile Xaa Xaa Glu Xaa Xaa Val Xaa Val Tyr Gly Phe Xaa Lys His  
210 215 220

Ile Arg Xaa Gln Arg Xaa Tyr Xaa Val Gln Thr Glu Glu Gln Tyr Xaa  
225 230 235 240

Phe Ile His Xaa Ala Leu Xaa Glu  
245

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Lys Ser Lys Asn Arg Asn Ser Asn Val Ile Pro Tyr Asp Tyr Asn  
1 5 10 15

Arg Val Pro Leu Lys His Glu Leu Glu Met Ser Lys Glu Ser Glu His  
20 25 30

Asp Ser Asp Glu Ser Ser Asp Asp Asp Ser Asp Ser Glu Glu Pro Ser  
35 40 45

Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser Tyr Trp Lys Pro Glu Val  
50 55 60

Met Ile Ala Ala Gln Gly Pro Leu Lys Glu Thr Ile Gly Asp Phe Trp  
65 70 75 80

Gln Met Ile Phe Gln Arg Lys Val Lys Val Ile Val Met Leu Thr Glu  
85 90 95

Leu Lys His Gly Asp Gln Glu Ile Cys Ala Gln Tyr Trp Gly Glu Gly  
100 105 110

Lys Gln Thr Tyr Gly Asp Ile Glu Val Asp Leu Lys Asp Thr Asp Lys  
115 120 125

Ser Ser Thr Tyr Thr Leu Arg Val Phe Glu Leu Arg His Ser Lys Arg  
130 135 140

Lys Asp Ser Arg Thr Val Tyr Gln Tyr Gln Tyr Thr Asn Trp Ser Val  
145 150 155 160

Glu Gln Leu Pro Ala Glu Pro Lys Glu Leu Ile Ser Met Ile Gln Val  
165 170 175

Val Lys Gln Lys Leu Pro Gln Lys Asn Ser Ser Glu Gly Asn Lys His  
180 185 190

His Lys Ser Thr Pro Leu Leu Ile His Cys Arg Asp Gly Ser Gln Gln  
195 200 205

Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu Leu Glu Ser Ala Glu Thr  
210 215 220

Glu Glu Val Val Asp Ile Phe Gln Val Val Lys Ala Leu Arg Lys Ala  
225 230 235 240

Arg Pro Gly Met Val Ser Thr Phe Glu Gln Tyr Gln Phe Leu Tyr Asp  
245 250 255

Val Ile Ala Ser  
260

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn  
1 5 10 15

Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val  
20 25 30

Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala  
35 40 45

Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile  
50 55 60

Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu  
65 70 75 80

Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val  
85 90 95

Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Cys Glu  
100 105 110

Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys  
115 120 125

Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly  
130 135 140

Ile Pro Ser Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln  
145 150 155 160

Lys Gln Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser  
165 170 175

Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu  
180 185 190

Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys  
195 200 205

Ser Leu Ala Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr  
210 215 220

Glu Phe Cys Tyr Lys Val Val Gln Glu  
225 230

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser  
1 5 10 15

Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn  
20 25 30

Ala Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr  
35 40 45

Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile Trp  
50 55 60

Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln Asn Met  
65 70 75 80

Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu Pro Ile Asn  
85 90 95

Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu His Lys Cys Leu  
100 105 110

Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe Ile Leu Glu Ala Thr  
115 120 125

Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys Trp  
130 135 140

Pro Asn Pro Asp Ser Pro Ile Ser Lys Thr Phe Glu Leu Ile Ser Val  
145 150 155 160

Ile Lys Glu Glu Ala Ala Asn Arg Asp Gly Pro Met Ile Val His Asp  
165 170 175

Glu His Gly Val Thr Ala Gly Thr Phe Cys Ala Leu Thr Thr Leu  
180 185 190

Met His Gln Leu Glu Lys Glu Asn Ser Val Asp Val Tyr Gln Val Ala  
195 200 205

Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln  
210 215 220

Tyr Gln Phe Leu Tyr Lys Val Ile Leu Ser  
225 230

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Val Val Pro Ser Glu Arg Ala  
1 5 10 15

Arg Val Gly Leu Ala Pro Leu Pro Gly Met Lys Gly Thr Asp Tyr Ile  
20 25 30

Asn Ala Ser Tyr Ile Met Gly Tyr Tyr Arg Ser Asn Glu Phe Ile Ile  
35 40 45

Thr Gln His Pro Leu Pro His Thr Thr Lys Asp Phe Trp Arg Met Ile  
50 55 60

Trp Asp His Asn Ala Gln Ile Ile Val Met Leu Pro Asp Asn Gln Ser  
65 70 75 80

Leu Ala Glu Asp Glu Phe Val Tyr Trp Pro Ser Arg Glu Glu Ser Met  
85 90 95

Asn Cys Glu Ala Phe Thr Val Thr Leu Ile Ser Lys Asp Arg Leu Cys  
100 105 110

Leu Ser Asn Glu Glu Gln Ile Ile His Asp Phe Ile Leu Glu Ala  
115 120 125

Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys  
130 135 140

Trp Pro Asn Pro Asp Ala Pro Ile Ser Ser Thr Phe Glu Leu Ile Asn  
145 150 155 160

Val Ile Lys Glu Glu Ala Leu Thr Arg Asp Gly Pro Thr Ile Val His  
165 170 175

Asp Glu Tyr Gly Ala Val Ser Ala Gly Met Leu Cys Ala Leu Thr Thr  
180 185 190

Leu Ser Gln Gln Leu Glu Asn Glu Asn Ala Val Asp Val Phe Gln Val  
195 200 205

Ala Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Thr Asp Ile Glu  
210 215 220

Gln Tyr Gln Phe Ile Tyr Lys Ala Arg Leu Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: /label= Xaa  
*/note= "For the Consensus Sequence, Xaa = Lack of Consensus"*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Xaa Ile Pro Tyr Glu Arg Asn  
1 5 10 15

Arg Val Gly Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu Gly Thr  
35 40 45

Asp Tyr Ile Asn Ala Ser Xaa Ile Met Gly Tyr Tyr Gln Ser Asn Glu  
50 55 60

Phe Ile Xaa Thr Gln Xaa Pro Leu Leu His Thr Ile Lys Asp Phe Trp  
65 70 75 80

Arg Met Ile Trp Asp His Xaa Asn Ala Gln Ile Val Met Leu Xaa Xaa  
85 90 95

Xaa Gln Xaa Xaa Ala Glu Xaa Glu Xaa Gln Tyr Trp Pro Ser Xaa  
100 105 110

Gly Xaa Xaa Xaa Tyr Gly Asp Xaa Xaa Val Xaa Leu Lys Xaa Xaa Xaa  
115 120 125

Asn Cys Glu Ser Xaa Thr Val Thr Xaa Xaa Xaa Glu Xaa Arg Xaa Cys  
130 135 140

Leu Ser Asn Glu Xaa Arg Xaa Ile Ile Gln Asp Phe Ile Leu Glu Ala  
145 150 155 160

Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys  
165 170 175

Trp Pro Asn Pro Asp Xaa Pro Ile Ser Xaa Thr Xaa Glu Leu Ile Ser  
180 185 190

Val Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Glu Glu Ala  
195 200 205

Xaa Asn Arg Xaa Xaa Xaa Asp Gly Pro Xaa Ile Val His Xaa Glu Xaa  
210 215 220

Gly Ala Val Xaa Xaa Gly Thr Phe Cys Ala Leu Thr Thr Leu Leu Glu  
225 230 235 240

Gln Leu Glu Xaa Glu Asn Xaa Val Asp Val Phe Gln Val Xaa Lys Met  
245 250 255

Xaa Asn Leu Met Arg Pro Gly Xaa Xaa Xaa Ile Glu Gln Tyr Gln  
260 265 270

Phe Leu Tyr Lys Val Ile Leu Ser  
275 280

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